# Accessing the dry matter yield persistence in an alfalfa germplasm within Brazil through random regression models

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Persistence plays a key role in alfalfa cultivation in tropical areas but is still a bottleneck for breeding programs. The objectives of study were to access the dry matter yield persistence of alfalfa accessions with a temperate genetic background evaluated under tropical conditions, and to propose a method for selecting persistent accessions based on Random Regression (RR) models using Artificial Neural Networks (ANN). Dry matter yield (DMY) taken from 24 harvest times was used to assess persistence. A RR model based on Legendre polynomials with a diagonal residual variance structure fitted persistence curves for each accession. The scores of the curves were clustered into four groups through k-means method. An ANN was adjusted to classify accessions based on the persistence groups established by the k-means algorithm. The fitted curves showed satisfactory amplitude regarding DMY overtime which suggest high persistence variability. K-means method accomplished 32 accessions in the 'High persistence' cluster, 29 in the 'Persistent', 12 in the 'Modest persistence', and four accessions in the 'Non-persistent' cluster. The apparent error rate of the persistence ANNs had 100% efficiency when classifying accessions in both training and validation steps. The three-step method for accessing persistence presented in this study included a (1) RR model to obtain persistence trends, a (2) k-means method to define different persistence clusters, and (3) an ANN to perform persistence classification in an automated way. The upside of this method is to evaluate different accessions using the same ANN. New accessions will be classified according to their genetic value scores using the same ANN previously fitted, with no need for a new clustering step. The persistence method jumps down

from three to two steps and can help alfalfa breeders in the decision-making process. The persistence method can support the selection of genotypes to compose base populations that will generate synthetic populations showing consistent DMY overtime.

Palavras-chave: *Medicago sativa*; genetic trajectory; artificial neural networks.